

# SEQUENCE LISTING

<110> Laus, Reiner  
Vidovic, Damir  
Graddis, Thomas

<120> Compositions and Methods for Dendritic  
Cell-Based Immunotherapy

<130> 7636-0022.30

<140> Not Yet Assigned

<141> Filed Herewith

<150> US 60/193,504

<151> 2000-03-30

<160> 30

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 555

<212> PRT

<213> Artificial Sequence

<220>

<223> HER500 construct

<400> 1

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Lys	Glu	Leu	Ala	Arg	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	35	40	45	
Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	50	55	60	
Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	65	70	75	80
Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	85	90	95	
Gln	Glu	Val	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	100	105	110	
Val	Pro	Leu	Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	115	120	125	
Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn	130	135	140	
Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	145	150	155	160
Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	165	170	175	
Asn	Pro	Gln	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	180	185	190	
His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser				



Gly	Phe	Leu	Phe	Leu	Leu	Phe	Phe	Trp	Leu	Asp	Arg	Ser	Val	Leu	Ala	
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Lys	Glu	Leu	Ala	Arg	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	
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Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	
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Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	
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Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	
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Gln	Glu	Val	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	
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Val	Pro	Leu	Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	
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Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	
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Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	
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His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	
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Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	
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		260					265						270			
Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	
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Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	
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Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	
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Pro	Ser	Glu	Gly	Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly	Asp	Leu	Gly	Met	
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Gly	Ala	Ala	Lys	Gly	Leu	Gln	Ser	Leu	Pro	Thr	His	Asp	Pro	Ser	Pro	
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Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	Thr	Val	Pro	Leu	Pro	Ser	Glu	Thr	
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Asp	Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val	
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Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg
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His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser
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Glu	Gln	Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu
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Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro
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Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr
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Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Ala	Ser	Ile	Ile	Asn	Phe	Glu
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Lys	Leu	Gly	Ala	Gly	Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser
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Thr	Arg	Ser	Gly	Gly	Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu
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Glu	Glu	Ala	Pro	Arg	Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser
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Asp	Val	Phe	Asp	Gly	Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	Gly	Leu	Gln
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Ser	Leu	Pro	Thr	His	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp
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Pro	Thr	Val	Pro	Leu	Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu
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Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg	Pro
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Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	Pro	Leu	Pro	Ala	Ala	Arg	Pro	Ala
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Gly	Ala	Thr	Leu	Glu	Arg	Ala	Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly
465					470					475					480
Val	Val	Lys	Asp	Val	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu
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Tyr	Leu	Thr	Pro	Gln	Gly	Gly	Ala	Ala	Pro	Gln	Pro	His	Pro	Pro	Pro
			500					505					510		
Ala	Phe	Ser	Pro	Ala	Phe	Asp	Asn	Leu	Tyr	Tyr	Trp	Asp	Gln	Asp	Pro
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Pro	Glu	Arg	Gly	Ala	Pro	Pro	Ser	Thr	Phe	Lys	Gly	Thr	Pro	Thr	Ala
	530					535					540				
Glu	Asn	Pro	Glu	Tyr	Leu	Gly	Leu	Asp	Val	Pro	Ala	Ala	Ala	His	His
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His	His	His	His												

<210> 4

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> HER500\*-rGM-CSF construct

<400> 4

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 20           25           30
Lys Glu Leu Ala Arg Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr
 35           40           45
Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
 50           55           60
Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu
 65           70           75           80
Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile
 85           90           95
Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln
100           105           110
Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu
115           120           125
Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn
130           135           140
Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln
145           150           155           160
Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg
165           170           175
Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe
180           185           190
His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser
195           200           205
Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp
210           215           220
Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala
225           230           235           240
Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His
245           250           255
Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu
260           265           270
Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro
275           280           285
Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro
290           295           300
Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr
305           310           315           320
Asn Tyr Leu Ser Thr Asp Val Gly Ser Ala Ser Ile Ile Asn Phe Glu
325           330           335
Lys Leu Gly Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser
340           345           350
Thr Arg Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu
355           360           365
Glu Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
370           375           380
Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln
385           390           395           400
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Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp  
 405 410 415  
 Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu  
 420 425 430  
 Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro  
 435 440 445  
 Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala  
 450 455 460  
 Gly Ala Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly  
 465 470 475 480  
 Val Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu  
 485 490 495  
 Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro  
 500 505 510  
 Ala Phe Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro  
 515 520 525  
 Pro Glu Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala  
 530 535 540  
 Glu Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Ala Ala Ala Pro Thr  
 545 550 555 560  
 Arg Ser Pro Asn Pro Val Thr Arg Pro Trp Lys His Val Asp Ala Ile  
 565 570 575  
 Lys Glu Ala Leu Ser Leu Leu Asn Asp Met Arg Ala Leu Glu Asn Glu  
 580 585 590  
 Lys Asn Glu Asp Val Asp Ile Ile Ser Asn Glu Phe Ser Ile Gln Arg  
 595 600 605  
 Pro Thr Cys Val Gln Thr Arg Leu Lys Leu Tyr Lys Gln Gly Leu Arg  
 610 615 620  
 Gly Asn Leu Thr Lys Leu Asn Gly Ala Leu Thr Met Ile Ala Ser His  
 625 630 635 640  
 Tyr Gln Thr Asn Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Ile Glu  
 645 650 655  
 Val Thr Thr Phe Glu Asp Phe Ile Lys Asn Leu Lys Gly Phe Leu Phe  
 660 665 670  
 Asp Ile Pro Phe Asp Cys Trp Lys Pro Val Gln Lys Gly Ala Pro Pro  
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 Pro Pro Ala His His His His His His  
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<210> 5

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> HER300\*-rGM-CSF construct

<400> 5

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 20 25 30  
 Lys Glu Leu Ala Arg Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr  
 35 40 45  
 Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met  
 50 55 60  
 Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu

65					70					75				80	
Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile
				85					90					95	
Gln	Glu	Val	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln
			100					105					110		
Val	Pro	Leu	Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu
		115					120					125			
Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn
		130				135					140				
Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln
145					150					155					160
Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg
			165						170					175	
Asn	Pro	Gln	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe
		180					185						190		
His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser
		195					200					205			
Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp
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Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala
225					230					235					240
Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His
			245						250					255	
Glu	Gln	Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu
			260					265					270		
Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro
		275					280					285			
Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro
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Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr
305					310					315					320
Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Ala	Ser	Ile	Ile	Asn	Phe	Glu
			325						330					335	
Lys	Leu	Ala	Ala	Pro	Thr	Arg	Ser	Pro	Asn	Pro	Val	Thr	Arg	Pro	Trp
		340					345						350		
Lys	His	Val	Asp	Ala	Ile	Lys	Glu	Ala	Leu	Ser	Leu	Leu	Asn	Asp	Met
		355					360					365			
Arg	Ala	Leu	Glu	Asn	Glu	Lys	Asn	Glu	Asp	Val	Asp	Ile	Ile	Ser	Asn
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Glu	Phe	Ser	Ile	Gln	Arg	Pro	Thr	Cys	Val	Gln	Thr	Arg	Leu	Lys	Leu
385					390					395					400
Tyr	Lys	Gln	Gly	Leu	Arg	Gly	Asn	Leu	Thr	Lys	Leu	Asn	Gly	Ala	Leu
			405						410					415	
Thr	Met	Ile	Ala	Ser	His	Tyr	Gln	Thr	Asn	Cys	Pro	Pro	Thr	Pro	Glu
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Thr	Asp	Cys	Glu	Ile	Glu	Val	Thr	Phe	Glu	Asp	Phe	Ile	Lys	Asn	
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Leu	Lys	Gly	Phe	Leu	Phe	Asp	Ile	Pro	Phe	Asp	Cys	Trp	Lys	Pro	Val
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Gln	Lys	Gly	Ala	Pro	Pro	Pro	Pro	Ala	His	His	His	His	His	His	
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<210> 6  
 <211> 1665  
 <212> DNA  
 <213> Artificial Sequence



<220>

<223> HER500 construct

<400> 6

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tgcaccaag	tgtgcaccgg	cacagacatg	aagctgcggc	tccctgccag	tcccgagacc	180
cacctggaca	tgctccgcca	cctctaccag	ggctgccagg	tggtgcaggg	aaacctggaa	240
ctcacctacc	tgcccaccaa	tgccagcctg	tccttcctgc	aggatatcca	ggaggtgcag	300
ggctacgtgc	tcatcgctca	caaccaagtg	aggcaggtcc	cactgcagag	gctgcggatt	360
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ccgctgaaca	ataccacccc	tgtcacaggg	gcctccccag	gaggcctgcg	ggagctgcag	480
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cctcctcctg	ccttcagccc	agccttcgac	aacctctatt	actgggacca	ggacccacca	1560
gagcgggggg	ctccaccagg	caccttcaaa	gggacaccta	cggcagagaa	cccagagtac	1620
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<210> 7

<211> 2070

<212> DNA

<213> Artificial Sequence

<220>

<223> HER500-hGM-CSF construct

<400> 7

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tgcaccaag	tgtgcaccgg	cacagacatg	aagctgcggc	tccctgccag	tcccgagacc	180
cacctggaca	tgctccgcca	cctctaccag	ggctgccagg	tggtgcaggg	aaacctggaa	240
ctcacctacc	tgcccaccaa	tgccagcctg	tccttcctgc	aggatatcca	ggaggtgcag	300
ggctacgtgc	tcatcgctca	caaccaagtg	aggcaggtcc	cactgcagag	gctgcggatt	360
gtgcgaggca	cccagctctt	tgaggacaac	tatgccctgg	ccgtgctaga	caatggagac	420
ccgctgaaca	ataccacccc	tgtcacaggg	gcctccccag	gaggcctgcg	ggagctgcag	480
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<210> 8

<211> 1692

<212> DNA

<213> Artificial Sequence

<220>

<223> HER500\* construct

<400> 8

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cacctggaca	tgtctcccca	cctctaccag	ggctgccagg	tgggtgcagg	aaacctggaa	240
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catcaccatc ac 1692

<210> 9

<211> 2091

<212> DNA

<213> Artificial Sequence

<220>

<223> HER500\*-rGM-CSF construct

<400> 9

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tcgacccaag tgtgcaccgg cacagacatg aagctgcggc tccctgccag tcccagacc      180
cacctggaca tgetccgcca cctctaccag ggctgccagg tggcgaggg aaacctggaa      240
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ccgctgaaca ataccacccc tgtcacaggg gcctccccag gaggcctgcg ggagctgcag      480
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tgctaccagg acacgatttt gtggaaggac atcttcaca agaacaacca gctggctctc      600
acactgatag acaccaaccg ctctcgggcc tgccaccctt gttctccgat gtgtaagggc      660
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gaggatttca taaagaacct taaaggcttt ctgtttgata tcccttttga ctgctggaag      2040
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<210> 10

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> HER300\*-rGM-CSF construct

<400> 10

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tcgaccaag tgtgcaccgg cacagacatg aagctgcggc tccctgccag tcccgagacc      180
cacctggaca tgctccgcca cctctaccag ggctgccagg tgggtgcagg aaacctggaa      240
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gtgcgaggca ccagctcttt tgaggacaac tatgccctgg ccgtgctaga caatggagac      420
ccgctgaaca ataccacccc tgtcacaggg gcctccccag gaggcctgcg ggagctgcag      480
cttcgaagcc tcacagagat cttgaaagga ggggtcttga tccagcggaa cccccagctc      540
tgctaccagg acacgatttt gtggaaggac atcttccaca agaacaacca gctggtctctc      600
aactgatag acaccaaccg ctctcggggc tgccacccct gttctccgat gtgtaagggc      660
tcccgtgct ggggagagag ttctgaggat tgtcagagcc tgacgcgcac tgtctgtgcc      720
ggtggctgtg cccgtgcaa ggggccactg cccactgact gctgccatga gcagtgtgct      780
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<210> 11
<211> 32
<212> PRT
<213> Homo sapiens

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<400> 11
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Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
          20             25             30

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<210> 12
<211> 3
<212> PRT
<213> Homo sapiens

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<400> 12
Lys Glu Leu
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<210> 13
<211> 3
<212> PRT
<213> Homo sapiens

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<400> 13
Gly Ala Ala
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<210> 14
<211> 2
<212> PRT

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<213> Artificial Sequence

<220>

<223> linker

<400> 14

Ala Arg

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<210> 15

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminal sequence of HER500 and HER500\* constructs

<400> 15

Ala Ala Ala His His His His His His

1

5

<210> 16

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminal sequence of HER500-hGM-CSF construct

<400> 16

Gly Ala Pro Pro Pro Pro Ala Ala Ala His His His His His His

1

5

10

15

<210> 17

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminal sequence of HER500\* and HER300\* rat GM-CSF constructs

<400> 17

Gly Ala Pro Pro Pro Pro Ala His His His His His His

1

5

10

<210> 18

<211> 127

<212> PRT

<213> Homo sapiens

<400> 18

Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val

1

5

10

15

Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr

20

25

30

Ala	Ala	Glu	Met	Asn	Glu	Thr	Val	Glu	Val	Ile	Ser	Glu	Met	Phe	Asp
	35						40					45			
Leu	Gln	Glu	Pro	Thr	Cys	Leu	Gln	Thr	Arg	Leu	Glu	Leu	Tyr	Lys	Gln
	50					55					60				
Gly	Leu	Arg	Gly	Ser	Leu	Thr	Lys	Leu	Lys	Gly	Pro	Leu	Thr	Met	Met
65				70					75					80	
Ala	Ser	His	Tyr	Lys	Gln	His	Cys	Pro	Pro	Thr	Pro	Glu	Thr	Ser	Cys
				85				90						95	
Ala	Thr	Gln	Ile	Ile	Thr	Phe	Glu	Ser	Phe	Lys	Glu	Asn	Leu	Lys	Asp
	100						105					110			
Phe	Leu	Leu	Val	Ile	Pro	Phe	Asp	Cys	Trp	Glu	Pro	Val	Gln	Glu	
	115						120					125			

<210> 19  
 <211> 381  
 <212> DNA  
 <213> Homo sapiens

<400> 19  
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 gaagtcattc cagaaatgtt tgacctccag gagccgacct gcctacagac ccgcctggag 180  
 ctgtacaagc agggcctgcg gggcagcctc accaagctca agggcccctt gaccatgatg 240  
 gccagccact acaagcagca ctgccctcca accccggaaa ctccctgtgc aaccagact 300  
 atcacctttg aaagtttcaa agagaacctg aaggactttc tgcttgatcat cccctttgac 360  
 tgctggggagc cagtccagga g 381

<210> 20  
 <211> 127  
 <212> PRT  
 <213> Rattus norvegicus

Ala	Pro	Thr	Arg	Ser	Pro	Asn	Pro	Val	Thr	Arg	Pro	Trp	Lys	His	Val
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Asp	Ala	Ile	Lys	Glu	Ala	Leu	Ser	Leu	Leu	Asn	Asp	Met	Arg	Ala	Leu
			20				25				30				
Glu	Asn	Glu	Lys	Asn	Glu	Asp	Val	Asp	Ile	Ile	Ser	Asn	Glu	Phe	Ser
		35				40					45				
Ile	Gln	Arg	Pro	Thr	Cys	Val	Gln	Thr	Arg	Leu	Lys	Leu	Tyr	Lys	Gln
	50				55					60					
Gly	Leu	Arg	Gly	Asn	Leu	Thr	Lys	Leu	Asn	Gly	Ala	Leu	Thr	Met	Ile
65				70				75						80	
Ala	Ser	His	Tyr	Gln	Thr	Asn	Cys	Pro	Pro	Thr	Pro	Glu	Thr	Asp	Cys
				85				90						95	
Glu	Ile	Glu	Val	Thr	Thr	Phe	Glu	Asp	Phe	Ile	Lys	Asn	Leu	Lys	Gly
	100						105					110			
Phe	Leu	Phe	Asp	Ile	Pro	Phe	Asp	Cys	Trp	Lys	Pro	Val	Gln	Lys	
	115						120					125			

<210> 21  
 <211> 381  
 <212> DNA  
 <213> Rattus norvegicus

<400> 21  
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ctatacaagc agggctctacg gggcaacctc accaaactca atggcgcctt gaccatgata 240
gccagccact accagacgaa ctgccctcca accccggaaa ctgactgtga aatagaagtc 300
accacctttg aggatttcac aaagaacctt aaaggctttc tgtttgatat cccttttgac 360
tgctggaagc cgggccagaa a 381

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<210> 22  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OVA-derived immunodominant octapeptide

<400> 22  
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 1 5

<210> 23  
 <211> 289  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
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 Ser Pro Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys  
 20 25 30  
 Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala  
 35 40 45  
 Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu  
 50 55 60  
 Ile Ala His Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile  
 65 70 75 80  
 Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu  
 85 90 95  
 Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser  
 100 105 110  
 Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu  
 115 120 125  
 Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp  
 130 135 140  
 Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn Asn Gln Leu Ala Leu  
 145 150 155 160  
 Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys Ser Pro  
 165 170 175  
 Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln  
 180 185 190  
 Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys Ala Arg Cys Lys Gly  
 195 200 205  
 Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys Ala Ala Gly Cys Thr  
 210 215 220  
 Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser  
 225 230 235 240  
 Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp  
 245 250 255

Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg Tyr Thr Phe Gly Ala  
 260 265 270  
 Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu Ser Thr Asp Val Gly  
 275 280 285  
 Ser

<210> 24  
 <211> 867  
 <212> DNA  
 <213> Homo sapiens

<400> 24  
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 ctcacctacc tgcccaccaa tgccagcctg tccttcctgc aggatatcca ggaggtgcag 180  
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 gtgcgaggca cccagctctt tgaggacaac tatgccctgg ccgtgctaga caatggagac 300  
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 cttcgaagcc tcacagagat cttgaaagga ggggtcttga tccagcggaa cccccagctc 420  
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 aactaccttt ctacggacgt gggatcc 867

<210> 25  
 <211> 217  
 <212> PRT  
 <213> Homo sapiens

<400> 25  
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 Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu  
 20 25 30  
 Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val  
 35 40 45  
 Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu  
 50 55 60  
 Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr  
 65 70 75 80  
 Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys  
 85 90 95  
 Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro  
 100 105 110  
 Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala  
 115 120 125  
 Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val  
 130 135 140  
 Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu  
 145 150 155 160  
 Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe  
 165 170 175



Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu  
180 185 190  
Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn  
195 200 205  
Pro Glu Tyr Leu Gly Leu Asp Val Pro  
210 215

<210> 26  
<211> 651  
<212> DNA  
<213> Homo sapiens

<400> 26  
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<210> 27  
<211> 397  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> NY-ESO-IC tumor antigen

<400> 27  
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20 25 30  
Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala  
35 40 45  
Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro  
50 55 60  
His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala  
65 70 75 80  
Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe  
85 90 95  
Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp  
100 105 110  
Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val  
115 120 125  
Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln  
130 135 140  
Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met  
145 150 155 160  
Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser  
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Gly Gln Arg Arg Gly Ala Gly Gly Met Val His His Arg His Arg Ser



<210> 29  
 <211> 1179  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SART-3-IC

<400> 29

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Lys	Ala	Gly	Pro	Lys	Ala	Asp	Gly	Glu	Glu	Asp	Glu	Val	Lys	Ala	Ala
			20					25					30		
Arg	Thr	Arg	Arg	Lys	Val	Leu	Ser	Arg	Ala	Val	Ala	Ala	Ala	Thr	Tyr
			35				40					45			
Lys	Thr	Met	Gly	Pro	Ala	Trp	Asp	Gln	Gln	Glu	Glu	Gly	Val	Ser	Glu
	50					55				60					
Ser	Asp	Gly	Asp	Glu	Tyr	Ala	Met	Ala	Ser	Ser	Ala	Glu	Ser	Ser	Pro
65					70				75						80
Gly	Glu	Tyr	Glu	Trp	Glu	Tyr	Asp	Glu	Glu	Glu	Glu	Lys	Asn	Gln	Leu
				85				90					95		
Glu	Ile	Glu	Arg	Leu	Glu	Glu	Gln	Leu	Ser	Ile	Asn	Val	Tyr	Asp	Tyr
			100				105					110			
Asn	Cys	His	Val	Asp	Leu	Ile	Arg	Leu	Leu	Arg	Leu	Glu	Gly	Glu	Leu
	115						120					125			
Thr	Lys	Val	Arg	Met	Ala	Arg	Gln	Lys	Met	Ser	Glu	Ile	Phe	Pro	Leu
	130					135					140				
Thr	Glu	Glu	Leu	Trp	Leu	Glu	Trp	Leu	His	Asp	Glu	Ile	Ser	Met	Ala
145					150					155					160
Gln	Asp	Gly	Leu	Asp	Arg	Glu	His	Val	Tyr	Asp	Leu	Phe	Glu	Lys	Ala
				165					170					175	
Val	Lys	Asp	Tyr	Ile	Cys	Pro	Asn	Ile	Trp	Leu	Glu	Tyr	Gly	Gln	Tyr
			180					185					190		
Ser	Val	Gly	Gly	Ile	Gly	Gln	Lys	Gly	Gly	Leu	Glu	Lys	Val	Arg	Ser
		195					200					205			
Val	Phe	Glu	Arg	Ala	Leu	Ser	Ser	Val	Gly	Leu	His	Met	Thr	Lys	Gly
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Leu	Ala	Leu	Trp	Glu	Ala	Tyr	Arg	Glu	Phe	Glu	Ser	Ala	Ile	Val	Glu
225					230				235						240
Ala	Ala	Arg	Leu	Glu	Lys	Val	His	Ser	Leu	Phe	Arg	Arg	Gln	Leu	Ala
				245					250					255	
Ile	Pro	Leu	Tyr	Asp	Met	Glu	Ala	Thr	Phe	Ala	Glu	Tyr	Glu	Glu	Trp
			260					265					270		
Ser	Glu	Asp	Pro	Ile	Pro	Glu	Ser	Val	Ile	Gln	Asn	Tyr	Asn	Lys	Ala
		275					280					285			
Leu	Gln	Gln	Leu	Glu	Lys	Tyr	Lys	Pro	Tyr	Glu	Glu	Ala	Leu	Leu	Gln
	290					295					300				
Ala	Glu	Ala	Pro	Arg	Leu	Ala	Glu	Tyr	Gln	Ala	Tyr	Ile	Asp	Phe	Glu
305					310					315					320
Met	Lys	Ile	Gly	Asp	Pro	Ala	Arg	Ile	Gln	Leu	Ile	Phe	Glu	Arg	Ala
				325					330					335	
Leu	Val	Glu	Asn	Cys	Leu	Val	Pro	Asp	Leu	Trp	Ile	Arg	Tyr	Ser	Gln
			340					345					350		
Tyr	Leu	Asp	Arg	Gln	Leu	Lys	Val	Lys	Asp	Leu	Val	Leu	Ser	Val	His
		355					360					365			
Asn	Arg	Ala	Ile	Arg	Asn	Cys	Pro	Trp	Thr	Val	Ala	Leu	Trp	Ser	Arg

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Tyr Leu Leu Ala Met Glu Arg His Gly Val Asp His Gln Val Ile Ser		
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Val Thr Phe Glu Lys Ala Leu Asn Ala Gly Phe Ile Gln Ala Thr Asp		400
	405	410
Tyr Val Glu Ile Trp Gln Ala Tyr Leu Asp Tyr Leu Arg Arg Arg Val		415
	420	425
Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu Arg Ala Ala		430
	435	440
Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu Glu Arg Phe		445
	450	455
Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn Trp Ala Arg		460
465	470	475
Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg Glu Leu Trp		480
	485	490
Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn Met Trp Leu		495
	500	505
Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln His Cys Arg		510
	515	520
Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr Pro Glu His		525
	530	535
Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly Ser Leu Glu		540
545	550	555
Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu Ala Arg Val		560
	565	570
Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala Leu Val Gln		575
	580	585
Gln Glu Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg Ala Glu Lys		590
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Lys Ala Leu Lys Lys Lys Lys Lys Ile Arg Gly Pro Glu Lys Arg Gly		605
610	615	620
Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu Glu Glu Gln		625
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Pro Ser Lys Arg Arg Arg Val Glu Asn Ser Ile Pro Ala Ala Gly Glu		640
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Thr Gln Asn Val Glu Val Ala Ala Gly Pro Ala Gly Lys Cys Ala Ala		655
	660	665
Val Asp Val Glu Pro Pro Ser Lys Gln Lys Glu Lys Ala Ala Ser Leu		670
	675	680
Lys Arg Asp Met Pro Lys Val Leu His Asp Ser Ser Lys Asp Ser Ile		685
690	695	700
Thr Val Phe Val Ser Asn Leu Pro Tyr Ser Met Gln Glu Pro Asp Thr		705
	710	715
Lys Leu Arg Pro Leu Phe Glu Ala Cys Gly Glu Val Val Gln Ile Arg		720
	725	730
Pro Ile Phe Ser Asn Arg Gly Asp Phe Arg Gly Tyr Cys Tyr Val Glu		735
	740	745
Phe Lys Glu Glu Lys Ser Ala Leu Gln Ala Leu Glu Met Asp Arg Lys		750
	755	760
Ser Val Glu Gly Arg Pro Met Phe Val Ser Pro Cys Val Asp Lys Ser		765
	770	775
Lys Asn Pro Asp Phe Lys Val Phe Arg Tyr Ser Thr Ser Leu Glu Lys		780
785	790	795
His Lys Leu Phe Ile Ser Gly Leu Pro Phe Ser Cys Thr Lys Glu Glu		800
	805	810
Leu Glu Glu Ile Cys Lys Ala His Gly Thr Val Lys Asp Leu Arg Leu		815
	820	825
		830

Val Thr Asn Arg Ala Gly Lys Pro Lys Gly Leu Ala Tyr Val Glu Tyr  
 835 840 845  
 Glu Asn Glu Ser Gln Ala Ser Gln Ala Val Met Lys Met Asp Gly Met  
 850 855 860  
 Thr Ile Lys Glu Asn Ile Ile Lys Val Ala Ile Ser Asn Pro Pro Gln  
 865 870 875 880  
 Arg Lys Val Pro Glu Lys Pro Glu Thr Arg Lys Ala Pro Gly Gly Pro  
 885 890 895  
 Met Leu Leu Pro Gln Thr Tyr Gly Ala Arg Gly Lys Gly Arg Thr Gln  
 900 905 910  
 Leu Ser Leu Leu Pro Arg Ala Leu Gln Arg Pro Ser Ala Ala Ala Pro  
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 Gln Ala Glu Asn Gly Pro Ala Ala Ala Pro Ala Val Ala Ala Pro Ala  
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 Ala Thr Glu Ala Pro Lys Met Ser Asn Ala Asp Phe Ala Lys Leu Phe  
 945 950 955 960  
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 965 970 975  
 Thr Arg Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu  
 980 985 990  
 Glu Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser  
 995 1000 1005  
 Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln  
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 Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp  
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 Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro  
 1060 1065 1070  
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 Gly Ala Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly  
 1090 1095 1100  
 Val Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu  
 1105 1110 1115 1120  
 Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro  
 1125 1130 1135  
 Ala Phe Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro  
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<210> 30

<211> 3537

<212> DNA

<213> Artificial Sequence

<220>

<223> SART-3-IC

<400> 30

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cgggctgtgg	ccgctgcgac	atacaagacc	atggggccag	cgtgggatca	gcaggaggaa	180

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ctgctcaggc	tggaaagggg	gcttaccaag	gtgaggatgg	cccgccagaa	gatgagtga	420
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